

'Next NGS Challenge – Data Processing and Integration' Conference – Conference report



Ana Conesa¹, Erik Bongcam-Rudloff²

¹Centro de Investigación Príncipe Felipe, Valencia, Spain

²Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden

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The 'Next NGS Challenge – data processing and integration' Conference (held on 15-16 May 2013, in Valencia, Spain), a joint event of EU COST Action BM1006, SeqAhead, the Global Bioinformatics Network, EMBnet, the International Society for Computational Biology, ISCB, and the FP7 Project, STAtEgra, aims to become a dedicated, annual conference on cutting-edge Next Generation Sequencing (NGS) applications. The goal of the conference was to bring together interested users, computational biologists and bioinformaticians who face new challenges in high-throughput sequencing, and to feature new trends in NGS-based genome research.

The conference consisted of keynote lectures, contributed oral presentations and lively afternoon poster sessions. Submissions were selected on novel NGS applications/discoveries, algorithms for NGS data processing and integration, and efficient solutions for the management of massive volumes of sequence data. Abstracts from the conference are available as an *EMBnet journal* supplement (Vol.19, Suppl. A¹).

NGS is a highly parallelised approach for quickly and economically sequencing new genomes, re-sequencing large numbers of known genomes, rapidly investigating transcriptomes, analysing communities, etc., under different conditions.

¹ <http://journal.embnet.org/index.php/embnetjournal/issue/current/showtoc>



Leif Andersson



Janet Kelso

Producing data on an unprecedented scale, these techniques are now driving the generation of knowledge (especially in biomedicine and molecular life sciences) to new dimensions. The massive data volumes being generated by these new technologies require new data-handling and storage methods. Hence, the life science community urgently needs new and improved



Poster session

approaches to facilitate NGS data management and analysis. A 'moving target', this field requires that bioinformaticians, computer scientists and biomedical scientists join their expertise to bring NGS data management and analysis to new levels of efficiency and integration.

The conference was a true success in terms both of the high number of participants from a wide diversity of countries and backgrounds, and of the quality of the keynote and contributed talks. The conference achieved its main goal of joining together cutting-edge presentations in the newest applications of NGS to genome organisation (from the Neanderthal genome, to genomes of domesticated animals and of economically relevant crops), novel data-mining and integrative bioinformatics approaches, and high-performance computing solutions for the new challenges of massive sequencing. The format of the conference, with extensive breaks and poster

sessions, favoured communication and networking among participants. Local logistics were also undertaken professionally, with particular attention to the satisfaction of attendees.

Finally some comments from the participants: Ralph Vogelslang, PacBio, Germany – "Thank you so much already for organising this great conference. It was a real pleasure for me to participate and get the chance to listen to excellent talks. I hope that you will have the chance to set up another conference next year and hopefully we can meet there again latest". Javier Terol, IVIA, Spain – "It has been a great conference, especially the keynote speakers and the second day-morning session. Truly, it was awesome."

More information about the conference: <http://www.thenextngschallenge.org>.

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